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Figure 1

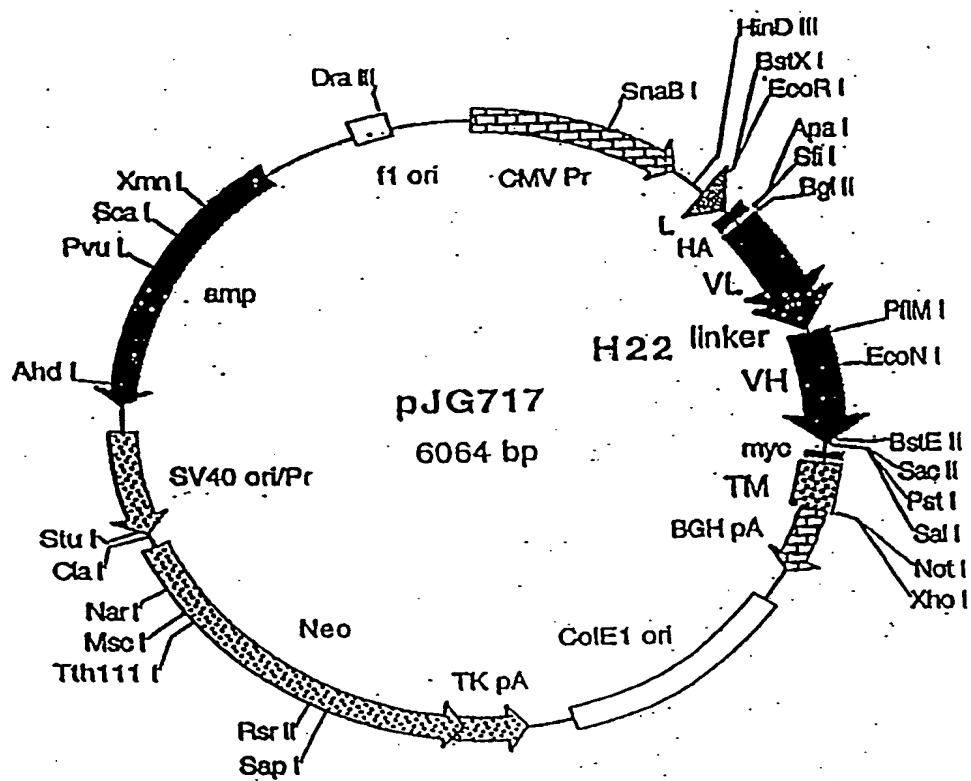
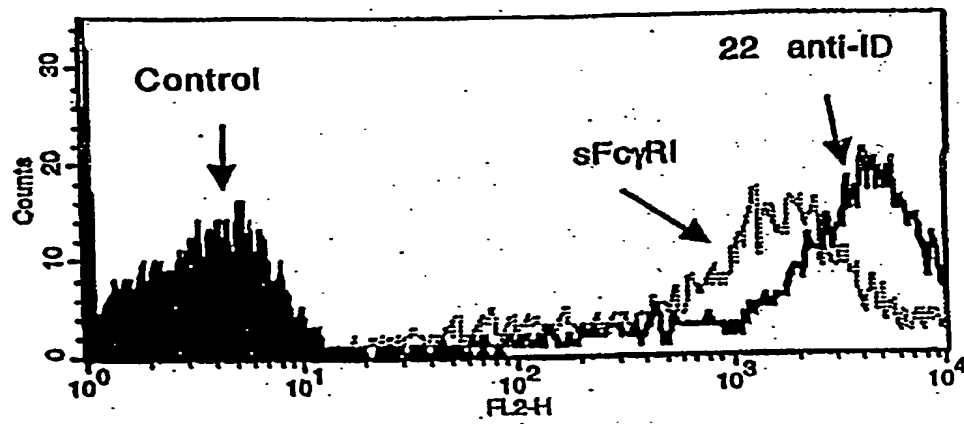


Figure 2.

NSO Cells



MTC Cells

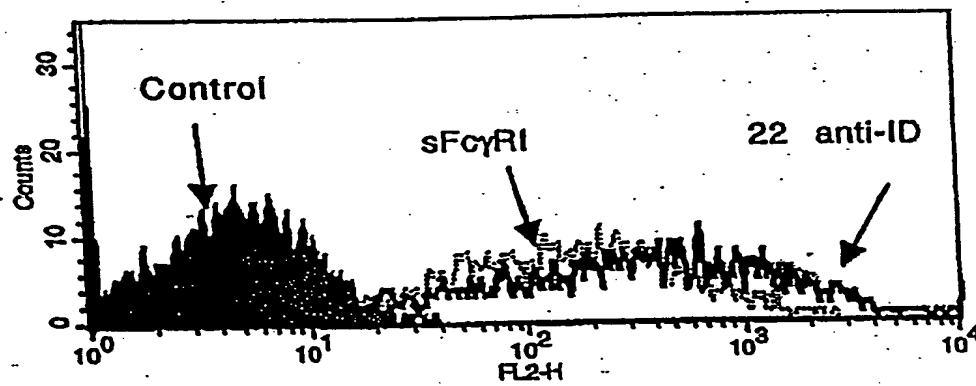
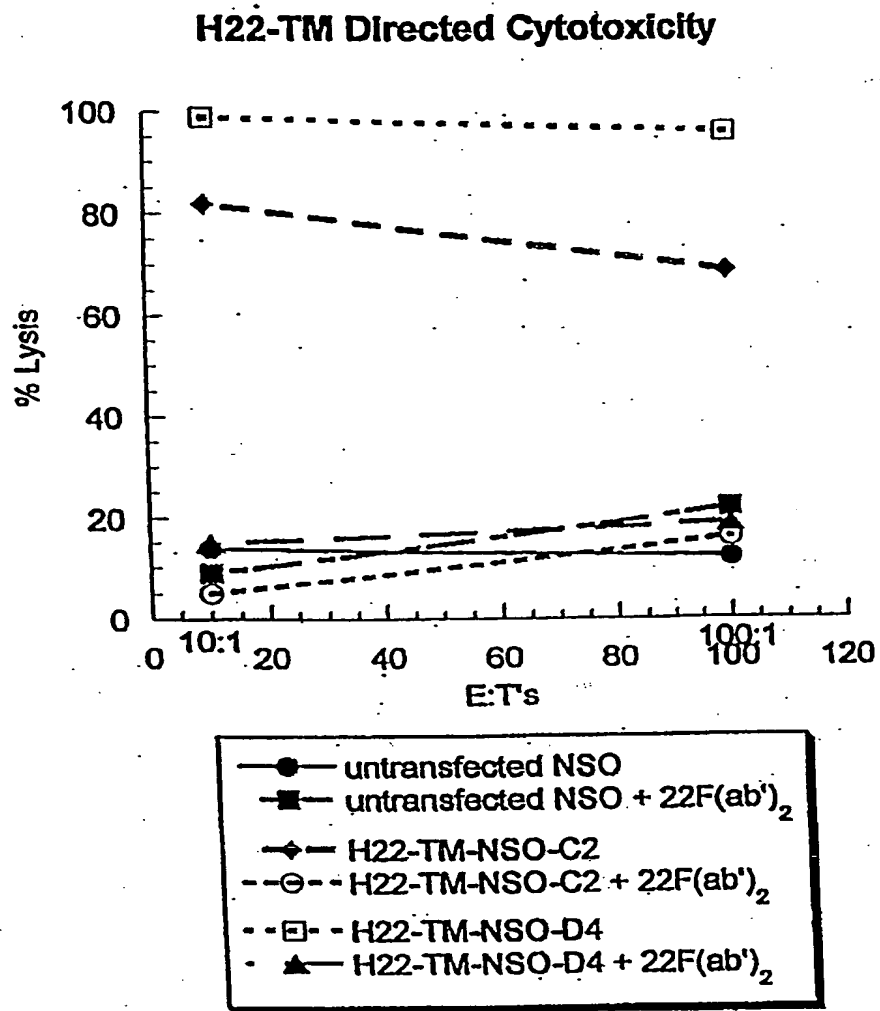


Figure 3.



Sequenc Range: 1 to 1132

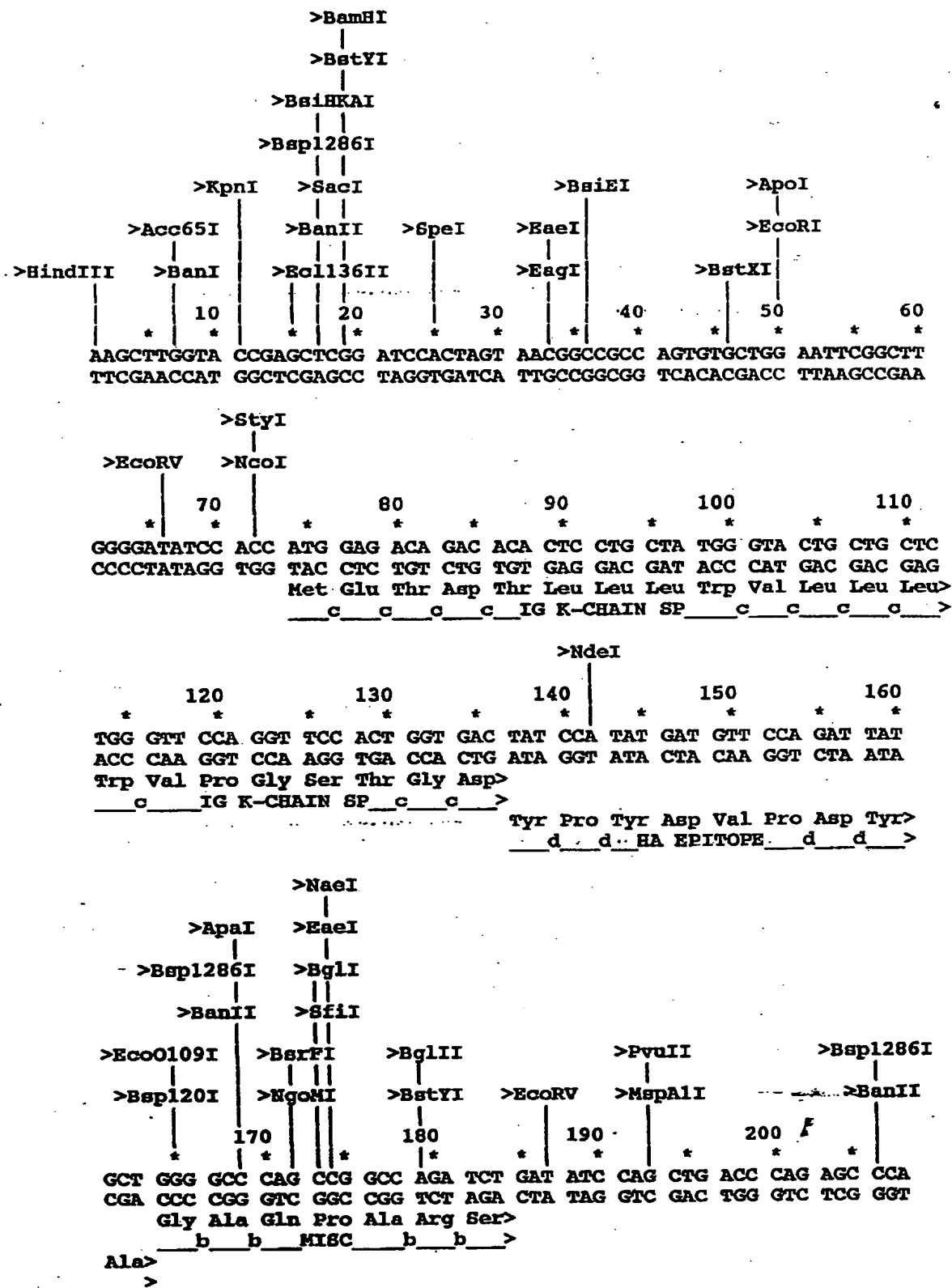


FIGURE 4A

Asp Ile Gln Leu Thr Gln Ser Pro>
 _____H22 VL_____>

>HaeII

210 220 230 240 250
 * * * * *
 AGC AGC CTG AGC GCC AGC GTG GGT GAC AGA GTG ACC ATC ACC TGT AAG
 TCG TCG GAC TCG CGG TCG CAC CCA CTG TCT CAC TGG TAG TGG ACA TTC
 Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys>
 _____H22 VL_____>

260 270 280 290 300
 * * * * *
 TCC AGT CAA AGT GTT TTA TAC AGT TCA AAT CAG AAG AAC TAC TTG GCC
 AGG TCA GTT TCA CAA AAT ATG TCA AGT TTA GTC TTC TTG ATG AAC CGG
 Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Gln Lys Asn Tyr Leu Ala>
 _____H22 VL_____>

>KpnI

>BamI

>Acc65I

310 320 330 340 350
 * * * * *
 TGG TAC CAG CAG AAG CCA GGT AAG GCT CCA AAG CTG CTG ATC TAC TGG
 ACC ATG GTC GTC TTC GGT CCA TTC CGA GGT TTC GAC GAC TAG ATG ACC
 Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Trp>
 _____H22 VL_____>

>MspAI

360 370 380 390 400
 * * * * *
 GCA TCC ACT AGG GAA TCT GGT GTG CCA AGC AGA TTC AGC GGT AGC GGT
 CGT AGG TGA TCC CTT AGA CCA CAC GGT TCG TCT AAG TCG CCA TCG CCA
 Ala Ser Thr Arg Glu Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly>
 _____H22 VL_____>

>KpnI

>Acc65I

>BamI

>BpmI

410 420 430 440
 * * * *
 AGC GGT ACC GAC TTC ACC TTC ACC ATC AGC AGC CTC CAG CCA GAG GAC
 TCG CCA TGG CTG AAG TGG AAG TGG TAG TCG TCG GAG GTC GGT CTC CTG
 Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp>
 _____H22 VL_____>

>StyI

>BseRI

>BssSI

>EaeI

450 460 470 480 490
 * * * * *
 ATC GCC ACC TAC TAC TGC CAT CAA TAC CTC TCC TCG TGG ACG TTC GGC
 TAG CGG TGG ATG ATG ACG GTA GTT ATG GAG AGG AGC ACC TGC AAG CCG
 Ile Ala Thr Tyr Tyr Cys His Gln Tyr Leu Ser Ser Trp Thr Phe Gly>

FIGURE 4B

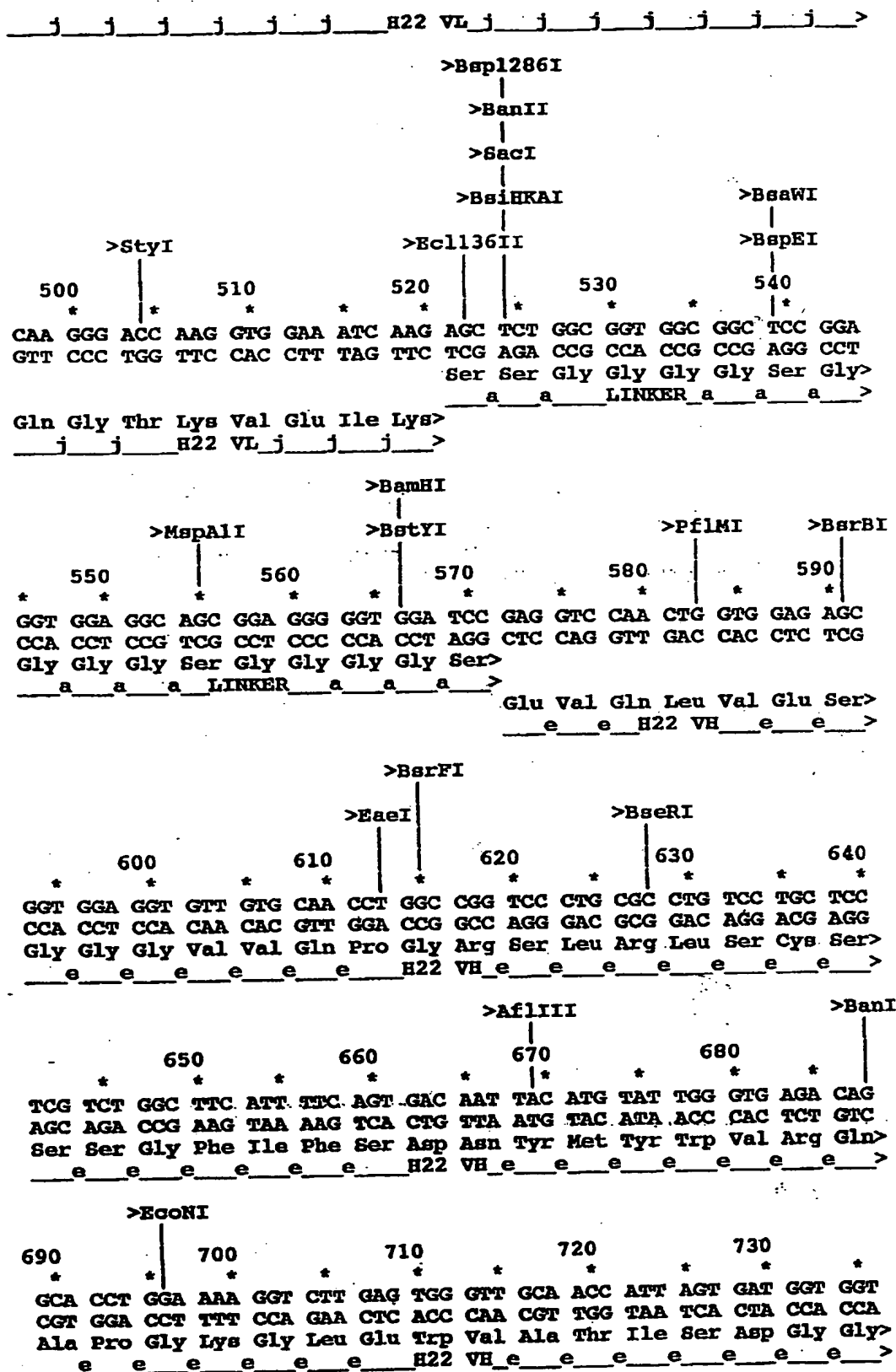


FIGURE 4C

FIGURE 4D


```

      980      |      990      |      1000      |      1010      |      1020
      *        |      *        |      *        |      *        |      *
CTG AAT GCT GTG GGC CAG GAC ACG CAG GAG GTC ATC GTG GTG CCA CAC
GAC TTA CGA CAC CCG GTC CTG TGC GTC CTC CAG TAG CAC CAC GGT GTG
  Asn>
  >
Leu>
  >
Ala Val Gly Gln Asp Thr Gln Glu Val Ile Val Val Pro His>
  _i_ _i_ _i_ _i_ _i_ PDGFR TM DOMAIN _i_ _i_ _i_ _i_ _i_ >

                                     >KcmI
                                     |
                                     >BglI
                                     |
      1030      |      1040      |      1050      |      1060      |      1070
      *        |      *        |      *        |      *        |      *
TCC TTG CCC TTT AAG GTG GTG GTG ATC TCA GCC ATC CTG GCC CTG GTG
AGG AAC GGG AAA TTC CAC CAC CAC TAG AGT CGG TAG GAC CGG GAC CAC
Ser Leu Pro Phe Lys Val Val Val Ile Ser Ala Ile Leu Ala Leu Val>
  _i_ _i_ _i_ _i_ _i_ _i_ PDGFR TM DOMAIN _i_ _i_ _i_ _i_ _i_ _i_ >

>BsiHKAI
|
>Bsp1286I
|
      1080      |      1090      |      1100      |      1110      |      1120
      *        |      *        |      *        |      *        |      *
GTG CTC ACC ATC ATC TCC CTT ATC ATC CTC ATC ATG CTT TGG CAG AAG
CAC GAG TGG TAG TAG AGG GAA TAG TAG GAG TAG TAC GAA ACC GTC TTC
Val Leu Thr Ile Ile Ser Leu Ile Ile Leu Ile Met Leu Trp Gln Lys>
  _i_ _i_ _i_ _i_ _i_ _i_ PDGFR TM DOMAIN _i_ _i_ _i_ _i_ _i_ _i_ >

      1130
      *        |      *
AAG CCA CGT T AG
TTC GGT GCA A TC
Lys Pro Arg>
  _i_ _i_ >

```

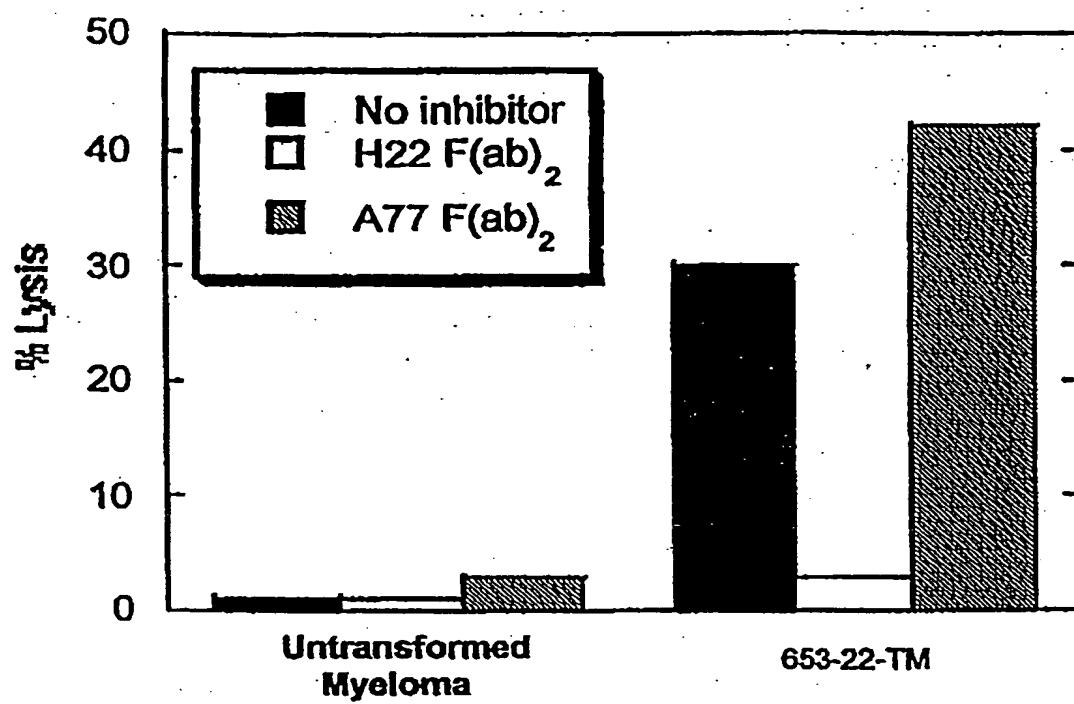


FIGURE 5

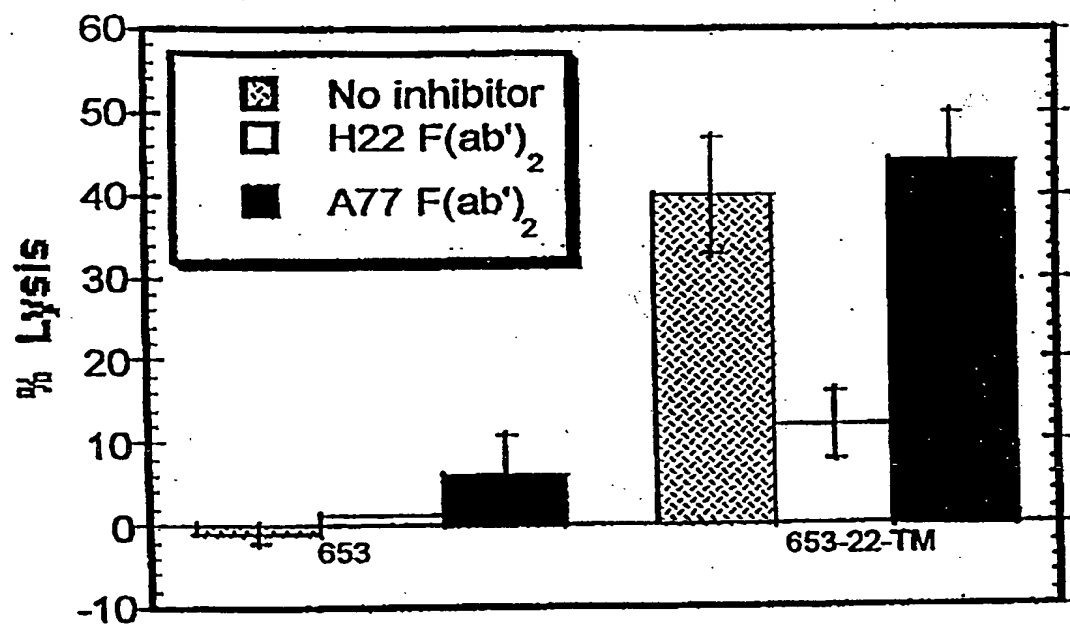


FIGURE 6

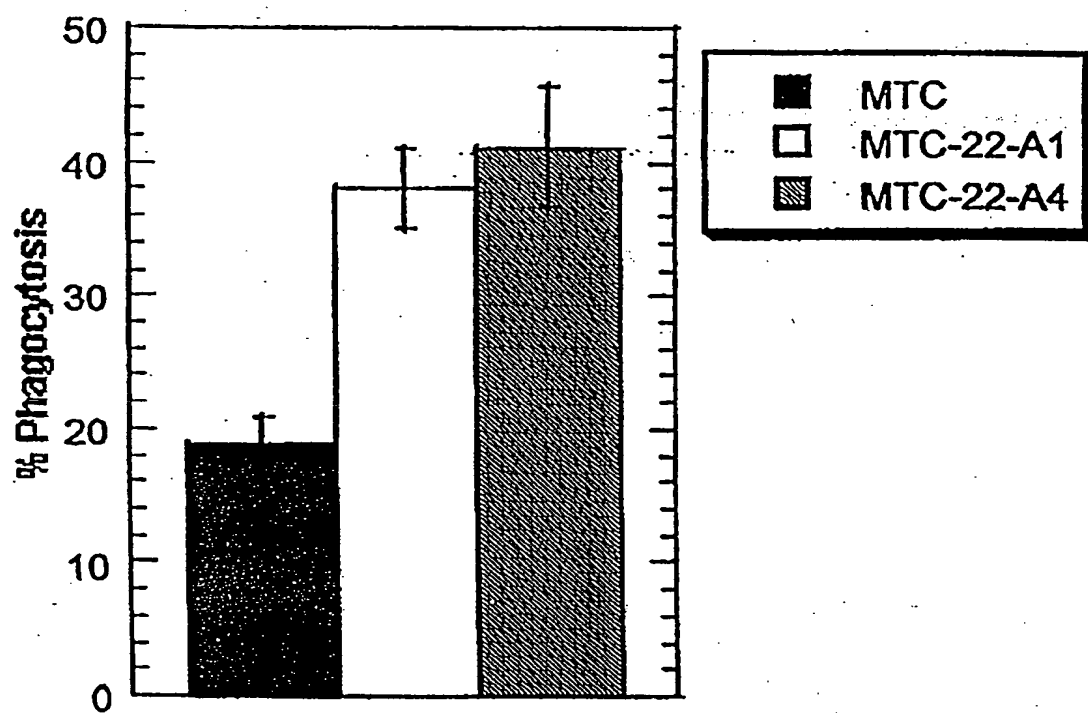


FIGURE 7

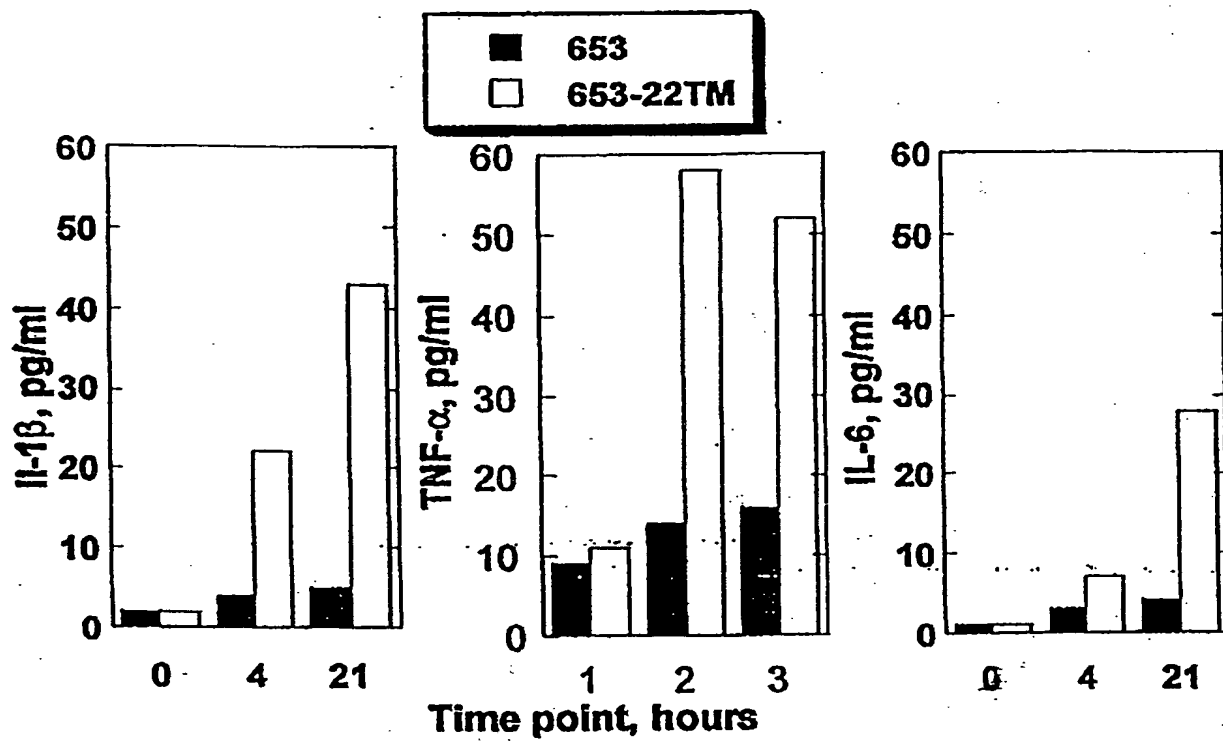


FIGURE 8

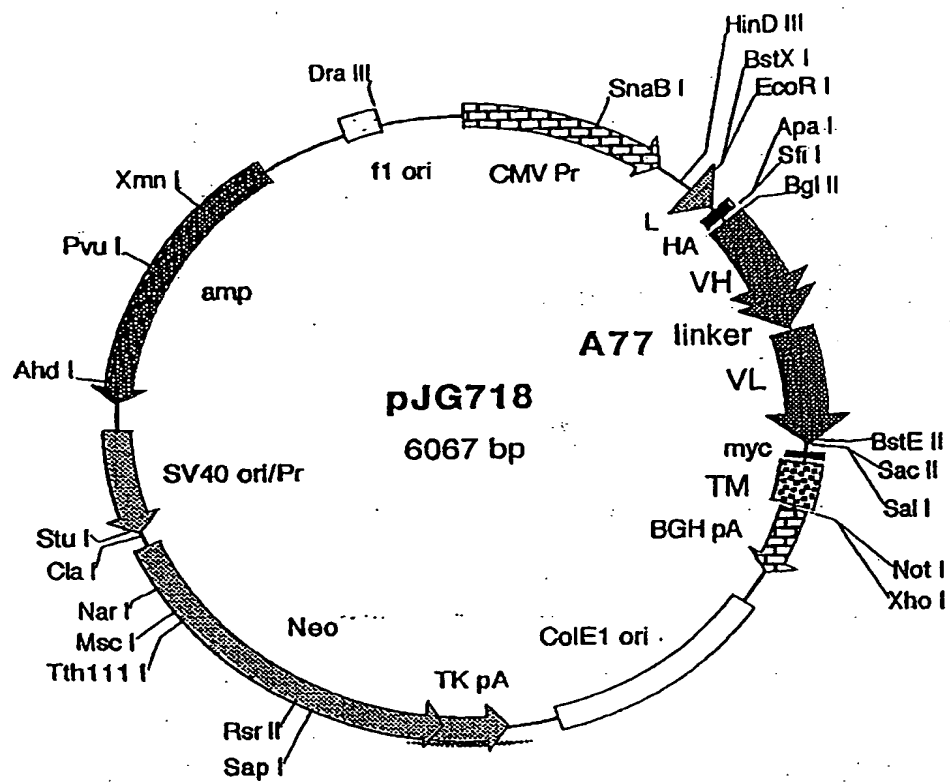


FIGURE 9

Sequence Range: 1 to 1135

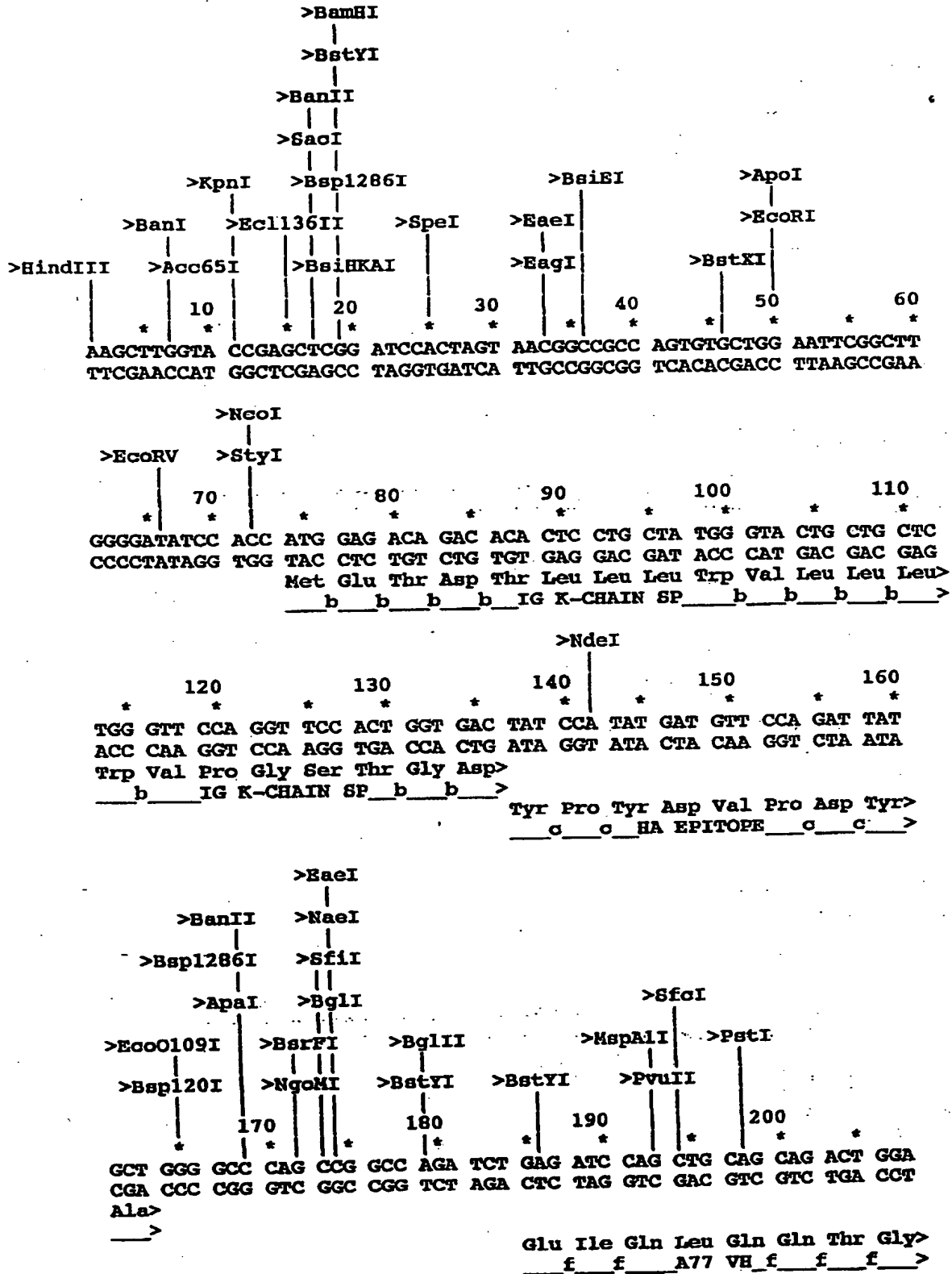


FIGURE 10A

Gly Ala Gln Pro Ala Arg Ser>
 _ _ _ _ MISC _ _ _ _ >

>Eco57I
 210 220 230 240 250
 * * * * *
 CCT GAG CTG GTG AAG CCT GGG GCT TCA GTG AAG ATA TCC TGC AAG GCT
 GGA CTC GAC CAC TTC GGA CCC CGA AGT CAC TTC TAT AGG ACG TTC CGA
 Pro Glu Leu Val Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala>
 _ f _ f _ f _ f _ f _ f _ A77 VH _ f _ f _ f _ f _ f _ f _ >

>EcoRV
 >NcoI
 >StyI

260 270 280 290 300
 * * * * *
 TCT GGT TAT TCA TTC ACT GAC TAC ATC ATA TTT TGG GTG AAG CAG AGC
 AGA CCA ATA AGT AAG TGA CTG ATG TAG TAT AAA ACC CAC TTC GTC TCG
 Ser Gly Tyr Ser Phe Thr Asp Tyr Ile Ile Phe Trp Val Lys Gln Ser>
 _ f _ f _ f _ f _ f _ f _ A77 VH _ f _ f _ f _ f _ f _ f _ >

>AseI
 >SspI

310 320 330 340 350
 * * * * *
 CAT GGA AAG AGC CTT GAG TGG ACT GGA AAT ATT AAT CCT TAC TAT GGT
 GTA CCT TTC TCG GAA CTC ACC TGA CCT TTA TAA TTA GGA ATG ATA CCA
 His Gly Lys Ser Leu Glu Trp Thr Gly Asn Ile Asn Pro Tyr Tyr Gly>
 _ f _ f _ f _ f _ f _ f _ A77 VH _ f _ f _ f _ f _ f _ f _ >

>ScaI
 >Eco57I
 >SfiI
 >AccI

360 370 380 390 400
 * * * * *
 AGT ACT AGC TAC AAT CTG AAG TTC AAG GGC AAG GCC ACA TTG ACT GTA
 TCA TGA TCG ATG TTA GAC TTC AAG TTC CCG TTC CGG TGT AAC TGA CAT
 Ser Thr Ser Tyr Asn Leu Lys Phe Lys Gly Lys Ala Thr Leu Thr Val>
 _ f _ f _ f _ f _ f _ f _ A77 VH _ f _ f _ f _ f _ f _ f _ >

410 420 430 440
 * * * *
 GAC AAA TCT TCC AGC ACA GCC TAC ATG CAG CTC AAC AGT CTG ACA TCT
 CTG TTT AGA AGG TCG TGT CGG ATG TAC GTC GAG TTG TCA GAC TGT AGA
 Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Asn Ser Leu Thr Ser>
 _ f _ f _ f _ f _ f _ f _ A77 VH _ f _ f _ f _ f _ f _ f _ >

>PstI
 >DrdI
 >SfiI
 >BseRI

450 460 470 480 490
 * * * * *
 GAG GAC TCT GCA GTC TAT TAC TGT GTA AGA GGA GTT TAT TAC TAC GGT
 CTC CTG AGA CGT CAG ATA ATG ACA CAT TCT CCT CAA ATA ATG ATG CCA
 Glu Asp Ser Ala Val Tyr Tyr Cys Val Arg Gly Val Tyr Tyr Tyr Gly>

FIGURE 10B


```

f f f f f f A77 VH f f f f f f f f >

                                     >StyI
500      510      520      530      540
*      *      *      *      *
AGT AGC TAC GAG GCG TTT CCT TAC TGG GGC CAA GGG ACT CTG GTC ACT
TCA TCG ATG CTC CGC AAA GGA ATG ACC CCG GTT CCC TGA GAC CAG TGA
Ser Ser Tyr Glu Ala Phe Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr>
f f f f f f A77 VH f f f f f f f f >

      >PstI      >BsaWI      >BseRI
      >SfoI      >BspEI      >MspAI
550      560      570      580      590
*      *      *      *      *
GTC TCT GCA GGA GGT GGC GGC TCC GGA GGA GGT GGC AGC GGA GGG GGC
CAG AGA CGT CCT CCA CCG CCG AGG CCT CCT CCA CCG TCG CCT CCC CCG
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly>
a a a a a LINKER a a a a a
Val Ser Ala>
f f >

>BamHI
>BstYI
600      610      620      630      640
*      *      *      *      *
GGA TCC GAT GTT GTG ATG ACC CAG ACT CCA CTC ACT TTG TCG ATT ACC
CCT AGG CTA CAA CAC TAC TGG GTC TGA GGT GAG TGA AAC AGC TAA TGG
Gly Ser>
a >
Asp Val Val Met Thr Gln Thr Pro Leu Thr Leu Ser Ile Thr>
g g g g g A77 VK g g g g g g g g >

650      660      670      680
*      *      *      *      *
ATT GGA CAA CCA GCC TCC ATC TCT TGC AAG TCA AGT CAG AGC CTC TTA
TAA CCT GTT GGT CGG AGG TAG AGA ACG TTC AGT TCA GTC TCG GAG AAT
Ile Gly Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Leu Leu>
g g g g g A77 VK g g g g g g g g >

690      700      710      720      730
*      *      *      *      *
GAT AGT GAT GGA AAG ACA TAT TTG AAT TGG TTG TTA CAG AGG CCA GGC
CTA TCA CTA CCT TTC TGT ATA AAC TTA ACC AAC AAT GTC TCC GGT CCG
Asp Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Arg Pro Gly>
g g g g g A77 VK g g g g g g g g >

                                     >DrdI
740      750      760      770      780
*      *      *      *      *
CAG TCT CCA ACG CGC CTA ATC TAT CTG GTG TCT AAA CTG GAG TCT GGA
GTC AGA GGT TGC GCG GAT TAG ATA GAC CAC AGA TTT GAC CTG AGA CCT
Gln Ser Pro Thr Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser Gly>
g g g g g A77 VK g g g g g g g g >

      >BpmI
790      800      810      820      830

```

FIGURE 10 C


```

                                >BglI
                                |
1030      1040      1050      1060      1070
*          *          *          *          *
CAC TCC TTG CCC TTT AAG GTG GTG GTG ATC TCA GCC ATC CTG GCC CTG
GTG AGG AAC GGG AAA TTC CAC CAC CAC TAG AGT CGG TAG GAC CGG GAC
His Ser Leu Pro Phe Lys Val Val Val Ile Ser Ala Ile Leu Ala Leu>
_e _e _e _e _e _e PDGFR TM DOMAIN_e _e _e _e _e _e _e >

>BsiHKAI
|
>Bsp1286I
|
1080      1090      1100      1110      1120
*          *          *          *          *
GTG GTG CTC ACC ATC ATC TCC CTT ATC ATC CTC ATC ATG CTT TGG CAG
CAC CAC GAG TGG TAG TAG AGG GAA TAG TAG GAG TAG TAC GAA ACC GTC
Val Val Leu Thr Ile Ile Ser Leu Ile Ile Leu Ile Met Leu Trp Gln>
_e _e _e _e _e _e PDGFR TM DOMAIN_e _e _e _e _e _e _e >

1130
*          *          *
AAG AAG CCA CGT TAG
TTC TTC GGT GCA ATC
Lys Lys Pro Arg>
PDGFR TM____>

```

FIGURE 10E

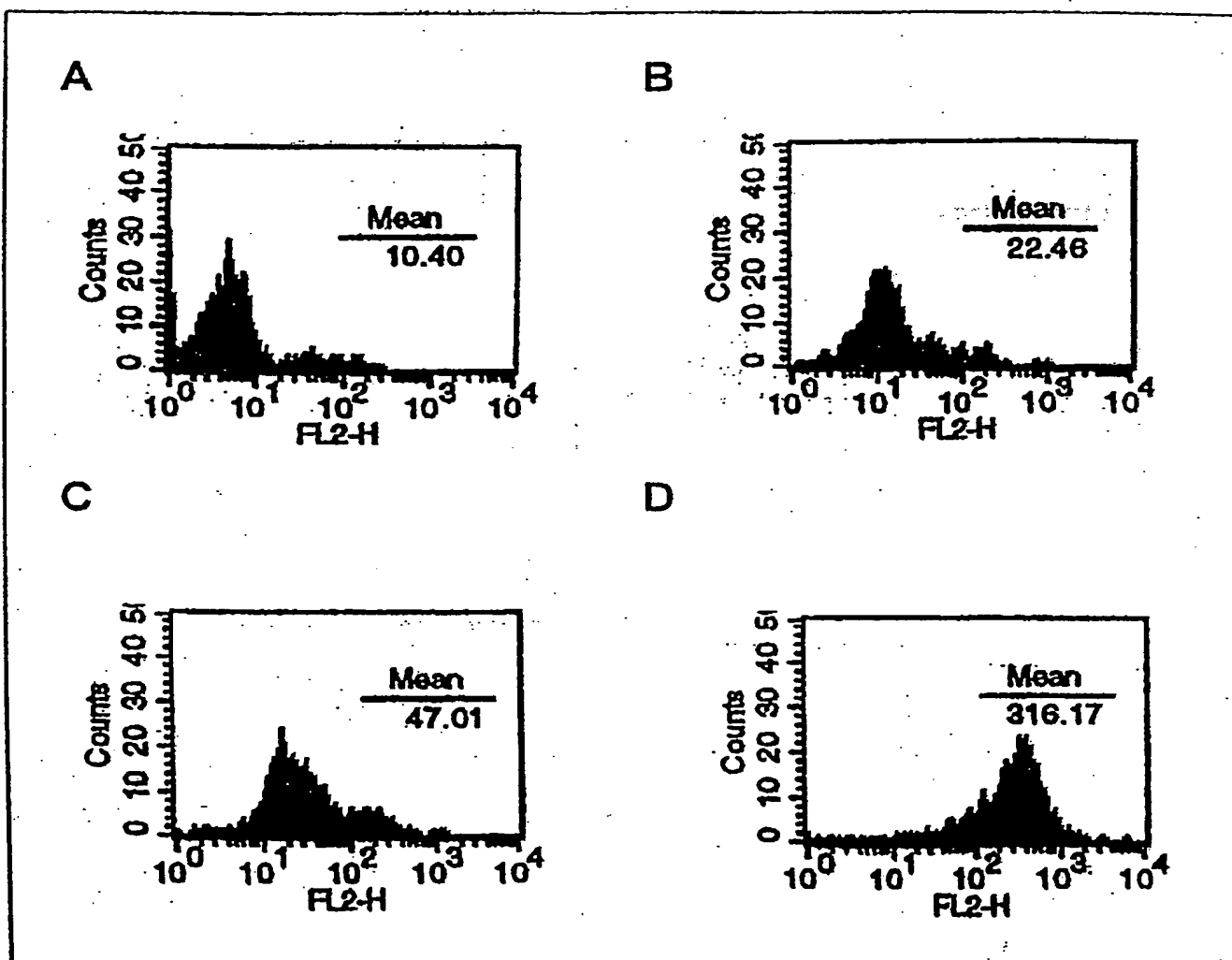


FIGURE II